> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                                    SEQUENCE LISTING
 2
 3  (1)    General Information:
 4    (i)APPLICANT:  GREENE, ET AL.
 5
 6   (ii)TITLE OF INVENTION:Human Tumor Necrosis Factor Receptor
 7
 8  (iii)NUMBER OF SEQUENCES:   9
 9
10   (iv)CORRESPONDENCE ADDRESS:
11
12  (A) ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
13        CECCHI, STEWART & OLSTEIN
14  (B) STREET:  6 BECKER FARM ROAD
15  (C) CITY:    ROSELAND
16  (D) STATE:   NEW JERSEY
17  (E) COUNTRY: USA
18  (F) ZIP:     07068
19
20   (v)COMPUTER READABLE FORM:
21  (A) MEDIUM TYPE:  3.5 INCH DISKETTE
22  (B) COMPUTER:  IBM PS/2
23  (C) OPERATING SYSTEM:  MS-DOS
24  (D) SOFTWARE:  WORD PERFECT 5.1
25
26   (vi)CURRENT APPLICATION DATA:
27  (A) APPLICATION NUMBER: 08/469,637
28  (B) FILING DATE: June 6, 1995
29  (C) CLASSIFICATION:
30
31  (vii)PRIOR APPLICATION DATA
32       (A)   APPLICATION NUMBER: PCT/US95/03216
33       (B)   FILING DATE: 15 MAR 95
34
35
36  (viii) ATTORNEY/AGENT INFORMATION:
37  (A) NAME:  FERRARO, GREGORY D.
38  (B) REGISTRATION NUMBER:  36,134
39  (C) REFERENCE/DOCKET NUMBER:  325800-381
40
41   (ix)TELECOMMUNICATION INFORMATION:
42  (A) TELEPHONE:  201-994-1700
43  (B) TELEFAX:    201-994-1744
44
45  (2) INFORMATION FOR SEQ ID NO:1:
46
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ENTERED

INPUT SET: S8513.raw

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47      (i) SEQUENCE CHARACTERISTICS:
48    (A) LENGTH:  1173 BASE PAIRS
49    (B) TYPE:  NUCLEIC ACID
50    (C) STRANDEDNESS:  SINGLE
51    (D) TOPOLOGY:  LINEAR
52
53    (ii) MOLECULE TYPE:  cDNA
54
55    (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:1:
56
57    ATGAACAAGT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC     60
58    CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG    120
59    TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC    180
60    GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT    240
61    CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC    300
62    CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA    360
63    CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG AACCCCAGA GCGAAATACA    420
64    GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCTGT    480
65    AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA    540
66    CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC    600
67    CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT    660
68    AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA    720
69    AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG AAACATCAA    780
70    AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC    840
71    GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA    900
72    AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA    960
73    CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC   1020
74    ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCACAAAC   1080
75    TGTCACTCAG AGTCTAAAGA AGACCATCAG GTTCCTTCAC AGCTTCACAA TGTACAAATT   1140
76    GTATCAGAAG TTATTTTTAG AAATGATAGG TAA                               1173
77
78    (2) INFORMATION FOR SEQ ID NO:2:
79    (i) SEQUENCE CHARACTERISTICS:
80    (A) LENGTH:  390 AMINO ACIDS
81    (B) TYPE:  AMINO ACID
82    (C) STRANDEDNESS:
83    (D) TOPOLOGY:  LINEAR
84
85    (ii) MOLECULE TYPE:  PROTEIN
86
87    (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:2:
88
89    Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
90        -20             -15                 -10
91    Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
92        -5               1               5
93    Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
94    10               15                  20
95    Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
96    25               30                  35
97    Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
98    40               45                  50
99    Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
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INPUT SET: S8513.raw

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100   55                    60                    65
101   Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
102   70                    75                    80
103   Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
104   85                    90                    95
105   His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
106   100                   105                   110
107   Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe
108   115                   120                   125
109   Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
110   130                   135                   140
111   Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr
112   145                   150                   155
113   His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
114   160                   165                   170
115   Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala
116   175                   180                   185
117   Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp
118   190                   195                   200
119   Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
120   205                   210                   215
121   Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys
122   220                   225                   230
123   Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile
124   235                   240                   245
125   Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile
126   250                   255                   260
127   Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu
128   265                   270                   275
129   Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr
130   280                   285                   290
131   Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser
132   295                   300                   305
133   Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu
134   310                   315                   320
135   Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Thr Asn
136   325                   330                   335
137   Cys His Ser Glu Ser Lys Glu Asp His Gln Val Pro Ser Gln Leu
138   340                   345                   350
139   His Asn Val Gln Ile Val Ser Glu Val Ile Phe Arg Asn Asp Arg
140   355                   360                   365
141
142   (2) INFORMATION FOR SEQ ID NO:3:
143
144      (i) SEQUENCE CHARACTERISTICS:
145   (A) LENGTH:   33 BASE PAIRS
146   (B) TYPE:  NUCLEIC ACID
147   (C) STRANDEDNESS:   SINGLE
148   (D) TOPOLOGY:   LINEAR
149
150      (ii) MOLECULE TYPE:  Oligonucleotide
151
152      (xi) SEQUENCE DESCRIPTION:   SEQ ID NO:3:
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/469,637*

INPUT SET: S8513.raw

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153
154     GCCAGAGGAT CCGAAACGTT TCCTCCAAAG TAC                          33
155
156     (2) INFORMATION FOR SEQ ID NO:4:
157
158       (i) SEQUENCE CHARACTERISTICS:
159     (A) LENGTH:  33 BASE PAIRS
160     (B) TYPE:  NUCLEIC ACID
161     (C) STRANDEDNESS:  SINGLE
162     (D) TOPOLOGY:  LINEAR
163
164       (ii) MOLECULE TYPE:  Oligonucleotide
165
166       (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:4:
167
168     CGGCTTCTAG AATTACCTAT CATTTCTAAA AAT                          33
169
170     (2) INFORMATION FOR SEQ ID NO:5:
171
172       (i) SEQUENCE CHARACTERISTICS:
173     (A) LENGTH:  31 BASE PAIRS
174     (B) TYPE:  NUCLEIC ACID
175     (C) STRANDEDNESS:  SINGLE
176     (D) TOPOLOGY:  LINEAR
177
178       (ii) MOLECULE TYPE:  Oligonucleotide
179
180       (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:5:
181
182     GCGCGGATCC ATGAACAAGT TGCTGTGCTG C                            31
183
184     (2) INFORMATION FOR SEQ ID NO:6:
185
186       (i) SEQUENCE CHARACTERISTICS:
187     (A) LENGTH:  34 BASE PAIRS
188     (B) TYPE:  NUCLEIC ACID
189     (C) STRANDEDNESS:  SINGLE
190     (D) TOPOLOGY:  LINEAR
191
192       (ii) MOLECULE TYPE:  Oligonucleotide
193
194       (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:6:
195
196     GCGCTCTAGA TTACCTATCA TTTCTAAAAA TAAC                         34
197
198     (2) INFORMATION FOR SEQ ID NO:7:
199
200       (i) SEQUENCE CHARACTERISTICS:
201     (A) LENGTH:  31 BASE PAIRS
202     (B) TYPE:  NUCLEIC ACID
203     (C) STRANDEDNESS:  SINGLE
204     (D) TOPOLOGY:  LINEAR
205
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206     (ii) MOLECULE TYPE:  Oligonucleotide
207
208     (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:7:
209
210   GCGCGGTACC TCAGTGGTTT GGGCTCCTCC C                        31
211
212   (2) INFORMATION FOR SEQ ID NO:8:
213
214      (i) SEQUENCE CHARACTERISTICS:
215   (A) LENGTH:  39 BASE PAIRS
216   (B) TYPE:  NUCLEIC ACID
217   (C) STRANDEDNESS:  SINGLE
218   (D) TOPOLOGY:  LINEAR
219
220     (ii) MOLECULE TYPE:  Oligonucleotide
221
222     (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:8:
223
224   GCCAGAGGAT CCGCCACCAT GAACAAGTTG CTGTGCTGC               39
225
226   (2) INFORMATION FOR SEQ ID NO:9:
227
228      (i) SEQUENCE CHARACTERISTICS:
229   (A) LENGTH:  60 BASE PAIRS
230   (B) TYPE:  NUCLEIC ACID
231   (C) STRANDEDNESS:  SINGLE
232   (D) TOPOLOGY:  LINEAR
233
234     (ii) MOLECULE TYPE:  Oligonucleotide
235
236     (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:9:
237
238   CGGCTTCTAG AATCAAGCGT AGTCTGGGAC GTCGTATGGG TACCTATCAT TTCTAAAAAT   60
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/469,637*

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Line   Error   Original Text